

### **Amendments to the Claims**

This listing of the claims will replace all prior versions, and listings, of claims in this application.

### **Listing of Claims**

1-26 (Canceled)

27. (Currently Amended) A method for determining the identity of an allelic variant of a 5-LO gene in a nucleic acid obtained from a patient, wherein the sample comprises a 5-LO gene sequence, comprising contacting a sample nucleic acid from the patient with a probe or primer having a sequence which is complementary to a 5-LO gene sequence, ~~wherein the probe or primer is selected from the group consisting of nucleic acids having a nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO:5, or SEQ ID NO:6, or the complement thereof, and~~ wherein the allelic variant comprises one or more nucleotide sequences selected from the group consisting of those set forth in SEQ ID NO: 4, SEQ ID NO:5, and SEQ ID NO:6, or the complements thereof, thereby determining the identity of the allelic variant.

28. (Original) The method of claim 27, wherein determining the identity of the allelic variant comprises determining the identity of at least one nucleotide at any one of the nucleotide residues selected from the group consisting of: residue 1000 of SEQ ID NO:1, any one of residues 472-477 of SEQ ID NO:1, and residue 559 of SEQ ID NO:1.

29. (Original) The method of claim 27, wherein determining the nucleotide content comprises sequencing the nucleotide sequence.

30. (Original) The method of claim 27, wherein determining the identity of the allelic variant comprises performing a restriction enzyme site analysis.

31. (Original) The method of claim 27, wherein determining the identity of the allelic variant is carried out by single-stranded conformation polymorphism.
32. (Original) The method of claim 27, wherein determining the identity of the allelic variant is carried out by allele specific hybridization.
33. (Original) The method of claim 27, wherein determining the identity of the allelic variant is carried out by primer specific extension.
34. (Original) The method of claim 27, wherein determining the identity of the allelic variant is carried out by an oligonucleotide ligation assay.
35. (Original) The method of claim 27, wherein the probe or primer comprises a nucleotide sequence from about 15 to about 30 nucleotides.
36. (Original) The method of claim 27, wherein the probe or primer is labeled.